

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Korenberg, Julie R.
Yamakawa, Kazuhiro
- (ii) TITLE OF INVENTION: A NOVEL CHROMOSOME 21 GENE MARKER,
COMPOSITIONS AND METHODS USING SAME
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CAMPBELL & FLORES, LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/337,690
 - (B) FILING DATE: 09-NOV-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-CE 2573
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: TRISOMY 21 FETAL BRAIN cDNA LIBRARY
 - (B) CLONE: EHOC-1
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: 21q22.3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 157..3729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAGGAAT CGGCACGAGG CGGCGCAACC GGCTCCGGAG CTGCCTGGCG CGGCCGGCG	60
GGCGCGCCG CTCAGGCTCG GGCTCCGGCT GGGCCCGGCG CGGCCTCGGG GCTGCCATG	120
GGGCGCGGGG GGCCGGCCG GTGACGCCGG ACCCCC ATG GAC GCC TCT GAG GAG Met Asp Ala Ser Glu Glu	174
1 5	
CCG CTG CCG CCG GTG ATC TAC ACC ATG GAG AAC AAG CCC ATC GTC ACC Pro Leu Pro Pro Val Ile Tyr Thr Met Glu Asn Lys Pro Ile Val Thr	222
10 15 20	
TGT GCT GGA GAT CAG AAT TTA TTT ACC TCT GTT TAT CCA ACG CTC TCT Cys Ala Gly Asp Gln Asn Leu Phe Thr Ser Val Tyr Pro Thr Leu Ser	270
25 30 35	
CAG CAG CTT CCA AGA GAA CCA ATG GAA TGG AGA AGG TCC TAT GGC CGG Gln Gln Leu Pro Arg Glu Pro Met Glu Trp Arg Arg Ser Tyr Gly Arg	318
40 45 50	
GCT CCG AAG ATG ATT CAC CTA GAG TCT AAC TTT GTT CAA TTC AAA GAG Ala Pro Lys Met Ile His Leu Glu Ser Asn Phe Val Gln Phe Lys Glu	366
55 60 65 70	
GAG CTG CTG CCC AAA GAA GGA AAC AAA GCT CTG CTC ACG TTT CCC TTC Glu Leu Leu Pro Lys Glu Gly Asn Lys Ala Leu Leu Thr Phe Pro Phe	414
75 80 85	
CTC CAT ATT TAC TGG ACA GAG TGC TGT GAT ACC GAA GTG TAT AAA GCT Leu His Ile Tyr Trp Thr Glu Cys Cys Asp Thr Glu Val Tyr Lys Ala	462
90 95 100	
ACA GTA AAA GAT GAC CTC ACC AAG TGG CAG AAT GTT CTG AAG GCT CAT Thr Val Lys Asp Asp Leu Thr Lys Trp Gln Asn Val Leu Lys Ala His	510
105 110 115	
AGC TCT GTG GAC TGG TTA ATA GTG ATA GTT GAA AAT GAT GCC AAG AAA Ser Ser Val Asp Trp Leu Ile Val Ile Val Glu Asn Asp Ala Lys Lys	558
120 125 130	
AAA AAC AAA ACC AAC ATC CTT CCC CGA ACC TCT ATT GTG GAC AAA ATA Lys Asn Lys Thr Asn Ile Leu Pro Arg Thr Ser Ile Val Asp Lys Ile	606
135 140 145 150	
AGA AAT GAT TTT TGT AAT AAA CAG AGT GAC AGG TGT GTT GTG CTC TCC Arg Asn Asp Phe Cys Asn Lys Gln Ser Asp Arg Cys Val Val Leu Ser	654
155 160 165	
GAC CCC TTG AAG GAC TCT TCT CGA ACT CAG GAA TCC TGG AAT GCC TTC Asp Pro Leu Lys Asp Ser Ser Arg Thr Gln Glu Ser Trp Asn Ala Phe	702
170 175 180	
CTG ACC AAA CTC AGG ACA TTG CTT CTT ATG TCT TTT ACC AAA AAC CTA Leu Thr Lys Leu Arg Thr Leu Leu Met Ser Phe Thr Lys Asn Leu	750
185 190 195	
GGC AAG TTT GAG GAT GAC ATG AGA ACC TTG AGG GAG AAG AGG ACT GAG Gly Lys Phe Glu Asp Asp Met Arg Thr Leu Arg Glu Lys Arg Thr Glu	798
200 205 210	
CCA GGC TGG AGC TTT TGT GAA TAT TTC ATG GTT CAG GAG GAG CTT GCC Pro Gly Trp Ser Phe Cys Glu Tyr Phe Met Val Gln Glu Glu Leu Ala	846
215 220 225 230	

TTT GTT TTC GAG ATG CTG CAG CAG TTC GAG GAC GCC CTG GTG CAG TAC Phe Val Phe Glu Met Leu Gln Gln Phe Glu Asp Ala Leu Val Gln Tyr 235 240 245	894
GAC GAA CTG GAC GCC CTC TTC TCT CAG TAT GTG GTC AAC TTC GGG GCC Asp Glu Leu Asp Ala Leu Phe Ser Gln Tyr Val Val Asn Phe Gly Ala 250 255 260	942
GGG GAT GGT GCC AAC TGG CTG ACT TTT TTC TGC CAG CCA GTG AAG AGC Gly Asp Gly Ala Asn Trp Leu Thr Phe Phe Cys Gln Pro Val Lys Ser 265 270 275	990
TGG AAC GGA TTG ATC CTC CGA AAA CCC ATA GAT ATG GAG AAG CGG GAA Trp Asn Gly Leu Ile Leu Arg Lys Pro Ile Asp Met Glu Lys Arg Glu 280 285 290	1038
TCG ATC CAG AGG CGA GAA GCC ACC CTG TTA GAT CTG CGC AGT TAC CTG Ser Ile Gln Arg Arg Glu Ala Thr Leu Leu Asp Leu Arg Ser Tyr Leu 295 300 305 310	1086
TTC TCT CGC CAG TGC ACC TTG CTG CTC TTC CTG CAG AGG CCG TGG GAG Phe Ser Arg Gln Cys Thr Leu Leu Phe Leu Gln Arg Pro Trp Glu 315 320 325	1134
GTG GCC CAG CGC GCC CTA GAG CTG CTG CAC AAC TGC GTG CAG GAA CTG Val Ala Gln Arg Ala Leu Glu Leu Leu His Asn Cys Val Gln Glu Leu 330 335 340	1182
AAG CTC TTA GAA GTC TCT GTC CCA CCT GGT GCT CTG GAC TGC TGG GTG Lys Leu Leu Glu Val Ser Val Pro Pro Gly Ala Leu Asp Cys Trp Val 345 350 355	1230
TTT CTG AGC TGT CTG GAG GTG TTG CAG AGG ATA GAA GGC TGC TGT GAC Phe Leu Ser Cys Leu Glu Val Leu Gln Arg Ile Glu Gly Cys Cys Asp 360 365 370	1278
CGG GCA CAG ATC GAC TCA AAC ATT GCC CAC ACT GTG GGG CTA TGG AGC Arg Ala Gln Ile Asp Ser Asn Ile Ala His Thr Val Gly Leu Trp Ser 375 380 385 390	1326
TAT GCC ACA GAA AAG TTA AAG TCC TTG GGC TAT CTA TGT GGA CTT GTG Tyr Ala Thr Glu Lys Leu Lys Ser Leu Gly Tyr Leu Cys Gly Leu Val 395 400 405	1374
TCA GAG AAA GGA CCT AAC TCA GAA GAT CTC AAC AGG ACA GTT GAC CTT Ser Glu Lys Gly Pro Asn Ser Glu Asp Leu Asn Arg Thr Val Asp Leu 410 415 420	1422
TTG GCA GGT TTG GGA GCT GAG CGA CCA GAA ACA GCC AAC ACA GCT CAG Leu Ala Gly Leu Gly Ala Glu Arg Pro Glu Thr Ala Asn Thr Ala Gln 425 430 435	1470
AGT CCT TAT AAG AAA CTG AAA GAA GCA TTA TCG TCA GTG GAA GCT TTT Ser Pro Tyr Lys Lys Leu Lys Glu Ala Leu Ser Ser Val Glu Ala Phe 440 445 450	1518
GAA AAA CAC TAC TTA GAT TTG TCC CAT GCC ACC ATT GAA ATG TAT ACA Glu Lys His Tyr Leu Asp Leu Ser His Ala Thr Ile Glu Met Tyr Thr 455 460 465 470	1566
AGC ATT GGG AGG ATT CGA TCT GCT AAG TTT GTT GGA AAA GAT CTG GCA Ser Ile Gly Arg Ile Arg Ser Ala Lys Phe Val Gly Lys Asp Leu Ala 475 480 485	1614
GAG TTT TAC ATG AGG AAA AAG GCT CCA CAA AAG GCA GAA ATC TAT CTT Glu Phe Tyr Met Arg Lys Lys Ala Pro Gln Lys Ala Glu Ile Tyr Leu 490 495 500	1662

CAA GGA GCA CTG AAA AAC TAC CTG GCT GAG GGC TGG GCA CTC CCC ATC Gln Gly Ala Leu Lys Asn Tyr Leu Ala Glu Gly Trp Ala Leu Pro Ile 505 510 515	1710
ACA CAC ACA AGG AAG CAG CTG GCC GAA TGT CAA AAG CAC CTT GGA CAA Thr His Thr Arg Lys Gln Leu Ala Glu Cys Gln Lys His Leu Gly Gln 520 525 530	1758
ATT GAA AAC TAC CTG CAG ACC AGC AGC CTC TTA GCC AGT GAC CAC CAC Ile Glu Asn Tyr Leu Gln Thr Ser Ser Leu Leu Ala Ser Asp His His 535 540 545 550	1806
CTC ACT GAA GAG GAG CGC AAG CAC TTC TGC CAG GAG ATA CTT GAC TTT Leu Thr Glu Glu Glu Arg Lys His Phe Cys Gln Glu Ile Leu Asp Phe 555 560 565	1854
GCC AGC CAG CCG TCA GAC AGC CCA GGT CAT AAG ATA GTG CTA CCC ATG Ala Ser Gln Pro Ser Asp Ser Pro Gly His Lys Ile Val Leu Pro Met 570 575 580	1902
CAT TCC TTT GCA CAA CTG CGA GAT CTC CAT TTT GAT CCC TCC AAT GCC His Ser Phe Ala Gln Leu Arg Asp Leu His Phe Asp Pro Ser Asn Ala 585 590 595	1950
GTG GTC CAC GTG GGC GGC GTT TTG TGC GTT GAG ATA ACC ATG TAC AGC Val Val His Val Gly Gly Val Leu Cys Val Glu Ile Thr Met Tyr Ser 600 605 610	1998
CAG ATG CCT GTG CCT GTT CAC GTG GAG CAG ATT GTG GTC AAT GTC CAC Gln Met Pro Val Pro Val His Val Glu Gln Ile Val Val Asn Val His 615 620 625 630	2046
TTC AGC ATT GAG AAA AAC AGC TAC CGG AAG ACT GCG GAG TGG CTT ACC Phe Ser Ile Glu Lys Asn Ser Tyr Arg Lys Thr Ala Glu Trp Leu Thr 635 640 645	2094
AAG CAC AAG ACG TCC AAT GGG ATC ATT AAC TTT CCA CCC GAG ACC GCA Lys His Lys Thr Ser Asn Gly Ile Ile Asn Phe Pro Pro Glu Thr Ala 650 655 660	2142
CCT TTC CCT GTA TCC CAA AAC AGT TTG CCC GCG CTG GAG TTG TAT GAA Pro Phe Pro Val Ser Gln Asn Ser Leu Pro Ala Leu Glu Leu Tyr Glu 665 670 675	2190
ATG TTT GAG AGA AGC CCA TCT GAT AAC TCC TTG AAC ACG ACT GGG ATT Met Phe Glu Arg Ser Pro Ser Asp Asn Ser Leu Asn Thr Thr Gly Ile 680 685 690	2238
ATC TGC AGA AAC GTC CAC ATG CTC CTG AGA AGG CAG GAG AGC AGC TCC Ile Cys Arg Asn Val His Met Leu Leu Arg Arg Gln Glu Ser Ser Ser 695 700 705 710	2286
TCT CTA GAG ATG CCC TCA GGG GTG GCT CTG GAG GAG GGT GCC CAC GTG Ser Leu Glu Met Pro Ser Gly Val Ala Leu Glu Glu Gly Ala His Val 715 720 725	2334
CTG AGG TGC AGC CAC GTG ACC CTG GAA CCA GGG GCC AAC CAG ATA ACA Leu Arg Cys Ser His Val Thr Leu Glu Pro Gly Ala Asn Gln Ile Thr 730 735 740	2382
TTC AGG ACT CAG GCC AAG GAA CCT GGA ACG TAT ACA CTC AGG CAG CTG Phe Arg Thr Gln Ala Lys Glu Pro Gly Thr Tyr Thr Leu Arg Gln Leu 745 750 755	2430
TGC GCC TCG GTG GGC TCC GTG TGG TTC GTC CTC CCT CAC ATC TAC CCC Cys Ala Ser Val Gly Ser Val Trp Phe Val Leu Pro His Ile Tyr Pro 760 765 770	2478

ATT GTG CAG TAC GAC GTG TAC TCA CAG GAG CCC CAG CTG CAC GTG GAG Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu Pro Gln Leu His Val Glu 775 780 785 790	2526
CCG CTG GCT GAT AGC CTT CTG GCA GGC ATT CCT CAG AGA GTC AAG TTC Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile Pro Gln Arg Val Lys Phe 795 800 805	2574
ACT GTC ACT ACC GGC CAT GAT ACG ATA AAG AAT GGA GAC AGC CTG CAG Thr Val Thr Gly His Asp Thr Ile Lys Asn Gly Asp Ser Leu Gln 810 815 820	2622
CTT AGC AAT GCC GAA GCC ATG CTC ATC CTG TGC CAG GCG GAG AGC AGG Leu Ser Asn Ala Glu Ala Met Leu Ile Leu Cys Gln Ala Glu Ser Arg 825 830 835	2670
GCT GTG GTC TAC TCC AAC ACG AGA GAA CAG TCT TCT GAG GCC GCG CTC Ala Val Val Tyr Ser Asn Thr Arg Glu Gln Ser Ser Glu Ala Ala Leu 840 845 850	2718
CGG ATT CAG TCC TCC GAC AAG GTC ACG AGC ATC AGT CTG CCT GTT GCG Arg Ile Gln Ser Ser Asp Lys Val Thr Ser Ile Ser Leu Pro Val Ala 855 860 865 870	2766
CCT GCG TAC CAC GTG ATC GAA TTT GAA CTG GAA GTT CTC TCT TTA CCT Pro Ala Tyr His Val Ile Glu Phe Glu Leu Glu Val Leu Ser Leu Pro 875 880 885	2814
TCA GCC CCA GCA CTC GGA GGG GAG AGT GAC ATG CTG GGG ATG GCA GAG Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp Met Leu Gly Met Ala Glu 890 895 900	2862
CCC CAC AGG AAG CAT AAG GAC AAA CAG AGA ACT GGC CGC TGC ATG GTT Pro His Arg Lys His Lys Asp Lys Gln Arg Thr Gly Arg Cys Met Val 905 910 915	2910
ACC ACA GAC CAC AAA GTG TCG ATT GAC TGC CCG TGG TCC ATC TAC TCC Thr Thr Asp His Lys Val Ser Ile Asp Cys Pro Trp Ser Ile Tyr Ser 920 925 930	2958
ACA GTC ATC GCA CTG ACC TTC AGC GTA CCC TTC AGG ACC ACA CAC AGC Thr Val Ile Ala Leu Thr Phe Ser Val Pro Phe Arg Thr Thr His Ser 935 940 945 950	3006
CTC CTG TCC TCA GGA ACA CGG AAA TAT GTT CAA GTT TGT GTC CAG AAT Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val Gln Val Cys Val Gln Asn 955 960 965	3054
TTG TCA GAA CTT GAC TTT CAG CTG TCA GAT AGT TAT CTT GTA GAT ACC Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp Ser Tyr Leu Val Asp Thr 970 975 980	3102
GGT GAT AGT ACC GAC CTG CAA CTA GTA CCA CTG AAC ACG CAG TCC CAG Gly Asp Ser Thr Asp Leu Gln Leu Val Pro Leu Asn Thr Gln Ser Gln 985 990 995	3150
CAG CCC ATC TAC AGC AAG CAG TCG GTG TTC TTC GTC TGG GAA CTC AAG Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe Phe Val Trp Glu Leu Lys 1000 1005 1010	3198
TGG ACA GAA GAG CCT CCC CCT TCT CTG CAT TGC CGG TTC TCT GTT GGA Trp Thr Glu Glu Pro Pro Ser Leu His Cys Arg Phe Ser Val Gly 1015 1020 1025 1030	3246
TTT TCC CCA GCT TCT GAG GAA CAG CTG TCT ATC TCC TTA AAG CCG TAT Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser Ile Ser Leu Lys Pro Tyr 1035 1040 1045	3294

ACT TAT GAA TTT AAA GTG GAA AAT TTT TTT ACA TTA TAC AAC GTG AAG	3342
Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe Thr Leu Tyr Asn Val Lys	
1050 1055 1060	
GCT GAG ATC TTT CCC CCT TCG GGA ATG GAG TAT TGC AGA ACA GGC TCC	3390
Ala Glu Ile Phe Pro Pro Ser Gly Met Glu Tyr Cys Arg Thr Gly Ser	
1065 1070 1075	
CTC TGC TCC CTG GAG GTT TTG ATC ACG AGG CTC TCA GAC CTC TTG GAG	3438
Leu Cys Ser Leu Glu Val Leu Ile Thr Arg Leu Ser Asp Leu Leu Glu	
1080 1085 1090	
GTG GAT AAA GAT GAA GCA CTG ACT GAA TCT GAT GAG CAT TTT TCG ACA	3486
Val Asp Lys Asp Glu Ala Leu Thr Glu Ser Asp Glu His Phe Ser Thr	
1095 1100 1105 1110	
AAG CTT ATG TAT GAA GTT GTC GAC AAC AGT AGC AAC TGG GCA GTG TGT	3534
Lys Leu Met Tyr Glu Val Val Asp Asn Ser Ser Asn Trp Ala Val Cys	
1115 1120 1125	
GGG AAA AGC TGC GGT GTC ATC TCC ATG CCA GTG GCT GCT CGG GCC ACT	3582
Gly Lys Ser Cys Gly Val Ile Ser Met Pro Val Ala Ala Arg Ala Thr	
1130 1135 1140	
CAC AGG GTC CAC ATG GAA GTG ATG CCG CTC TTC GCC GGG TAT CTC CCC	3630
His Arg Val His Met Glu Val Met Pro Leu Phe Ala Gly Tyr Leu Pro	
1145 1150 1155	
CTG CCC GAC GTC AGG CTG TTC AAG TAC CTC CCC CAT CAT TCT GCA CAC	3678
Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu Pro His His Ser Ala His	
1160 1165 1170	
TCC TCC CAA CTG GAC GCT GAC TGG ATA GAA AAC GCA GCC TGT CAG	3726
Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile Glu Asn Ala Ala Cys Gln	
1175 1180 1185 1190	
TAGACAAGCA CGGGGACGAC CAGCCGGACA GCAGCAGCCT CAAGAGCAGG GGCAGCGTGC	3786
ATTGGGCCTG CAGCAGCGAG CACAAAGGCC TACCCATGCC CCGGCTGCAG GCACTGCCGG	3846
CCGGCCAGGT CTTCAACTCC AGCTCGGGCA CACAAGTCCT GGTCTCATCCCC AGCCAAGATG	3906
ACCACGTCTT GGAAGTCAGT GTAACATGAC AACGCCAGGG TGAACACACG CCACCTCCCA	3966
GCTAGGAGTG CACTTTATGG GACTGTGACT GGACTCTTCC GTTCTGGCTC CAGCCAGACC	4026
TTCAGTGGTC CTGCCTGGCC GTGGGGACAT CAGAGAGTGT CATCACGCAG CTGGCCAGCT	4086
GAGTTCTGTT GTTGTGTTCA TGCCGCTGT GATCTCAGAT TCCTGCTTTT CTCACCCCGT	4146
CCCCATGCTG GTGTCCGACG CCGCTTACTC AGAGCCCTGG CCTCCCTCCC CCTACCTCAC	4206
ACGCTGCTCA TGAAAGTTTC CACCCACGCT GTCTCCACGG AACAGCCTCC GTCTGCTGGC	4266
TCTTCGTGGA AGGCCATTTG TCTTCAGGT AGACACTCAG CAGCCCTCAC GGTCTTAGTG	4326
ACGTGTGTGC CTTCTGGTC ACACAGCTGC CCAGTTCCCT GATCGGGGTG GATTTGTGTC	4386
CCCTAAGGGG TAAAACAGCC GTTTACCGCA GATCCTCTCA TACACCCCTTC TAGGGGAGGC	4446
GGGTGGGGGA GGGAGGGATC ATAACCCCTT CTGTGCCTTG GGATGCCGGA GCTGGGGGAC	4506
CTGGAGGCC ATCAGCCGGA GCCACGTGAA AGGTACTGAA GAAAGCTGAG ACCCGGCTGT	4566
GAGGAGCGCC TCAGCGGTGA GGTGGTTAG GGATAAAATGT TTCTGGAACC CTGTGGTCCC	4626
CCATAATGTT GATAGATATC ATATGCACTG GGAGTTAAAT ATATTAATT TAATGATCAT	4686

TATATATGTG GGGGTTAATA TGTGTTTTT CTGTCCTTT AAAGTCTTTA CATGTAATTG	4746
TAGCTGTATA ATCGTTATTT TTCTTTGCA TCTTAAGTCT TAGAAATTAA GATATTCCAT	4806
CGTGAGGATG AGAGAGGTCC TCAGTGTGTT TTTGGTCTGG TTGTAGGGAA GGACTCAAGT	4866
CCTGGAATGT CCTCCACTGG TCTACTGAGT TGCAGTCACA CTGTTCCAAT GGATTATTG	4926
CTTTCGGTTG TAAATTTAAT TGTACATATG GTTGATTTAT TATTTTAAA AATACAGACT	4986
AACTGATGTA ATGTTTATGT ATAAGTTGCA CCAAAAATCA AGGACAAAAAA TAAAGTGTGTT	5046
TGTTTTACA GGTGTGAAAG TCACAGCTTG TAAATAAGTG TTGTATGTAT TAAACCTTT	5106
CCAGTTCTCC AAAAAAAA AAAAAAAA AAAAAA	5141

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Ala Ser Glu Glu Pro Leu Pro Pro Val Ile Tyr Thr Met Glu	
1 5 10 15	
Asn Lys Pro Ile Val Thr Cys Ala Gly Asp Gln Asn Leu Phe Thr Ser	
20 25 30	
Val Tyr Pro Thr Leu Ser Gln Gln Leu Pro Arg Glu Pro Met Glu Trp	
35 40 45	
Arg Arg Ser Tyr Gly Arg Ala Pro Lys Met Ile His Leu Glu Ser Asn	
50 55 60	
Phe Val Gln Phe Lys Glu Glu Leu Leu Pro Lys Glu Gly Asn Lys Ala	
65 70 75 80	
Leu Leu Thr Phe Pro Phe Leu His Ile Tyr Trp Thr Glu Cys Cys Asp	
85 90 95	
Thr Glu Val Tyr Lys Ala Thr Val Lys Asp Asp Leu Thr Lys Trp Gln	
100 105 110	
Asn Val Leu Lys Ala His Ser Ser Val Asp Trp Leu Ile Val Ile Val	
115 120 125	
Glu Asn Asp Ala Lys Lys Asn Lys Thr Asn Ile Leu Pro Arg Thr	
130 135 140	
Ser Ile Val Asp Lys Ile Arg Asn Asp Phe Cys Asn Lys Gln Ser Asp	
145 150 155 160	
Arg Cys Val Val Leu Ser Asp Pro Leu Lys Asp Ser Ser Arg Thr Gln	
165 170 175	
Glu Ser Trp Asn Ala Phe Leu Thr Lys Leu Arg Thr Leu Leu Leu Met	
180 185 190	
Ser Phe Thr Lys Asn Leu Gly Lys Phe Glu Asp Asp Met Arg Thr Leu	
195 200 205	

Arg Glu Lys Arg Thr Glu Pro Gly Trp Ser Phe Cys Glu Tyr Phe Met
 210 215 220
 Val Gln Glu Glu Leu Ala Phe Val Phe Glu Met Leu Gln Gln Phe Glu
 225 230 235 240
 Asp Ala Leu Val Gln Tyr Asp Glu Leu Asp Ala Leu Phe Ser Gln Tyr
 245 250 255
 Val Val Asn Phe Gly Ala Gly Asp Gly Ala Asn Trp Leu Thr Phe Phe
 260 265 270
 Cys Gln Pro Val Lys Ser Trp Asn Gly Leu Ile Leu Arg Lys Pro Ile
 275 280 285
 Asp Met Glu Lys Arg Glu Ser Ile Gln Arg Arg Glu Ala Thr Leu Leu
 290 295 300
 Asp Leu Arg Ser Tyr Leu Phe Ser Arg Gln Cys Thr Leu Leu Leu Phe
 305 310 315 320
 Leu Gln Arg Pro Trp Glu Val Ala Gln Arg Ala Leu Glu Leu Leu His
 325 330 335
 Asn Cys Val Gln Glu Leu Lys Leu Leu Glu Val Ser Val Pro Pro Gly
 340 345 350
 Ala Leu Asp Cys Trp Val Phe Leu Ser Cys Leu Glu Val Leu Gln Arg
 355 360 365
 Ile Glu Gly Cys Cys Asp Arg Ala Gln Ile Asp Ser Asn Ile Ala His
 370 375 380
 Thr Val Gly Leu Trp Ser Tyr Ala Thr Glu Lys Leu Lys Ser Leu Gly
 385 390 395 400
 Tyr Leu Cys Gly Leu Val Ser Glu Lys Gly Pro Asn Ser Glu Asp Leu
 405 410 415
 Asn Arg Thr Val Asp Leu Leu Ala Gly Leu Gly Ala Glu Arg Pro Glu
 420 425 430
 Thr Ala Asn Thr Ala Gln Ser Pro Tyr Lys Lys Leu Lys Glu Ala Leu
 435 440 445
 Ser Ser Val Glu Ala Phe Glu Lys His Tyr Leu Asp Leu Ser His Ala
 450 455 460
 Thr Ile Glu Met Tyr Thr Ser Ile Gly Arg Ile Arg Ser Ala Lys Phe
 465 470 475 480
 Val Gly Lys Asp Leu Ala Glu Phe Tyr Met Arg Lys Lys Ala Pro Gln
 485 490 495
 Lys Ala Glu Ile Tyr Leu Gln Gly Ala Leu Lys Asn Tyr Leu Ala Glu
 500 505 510
 Gly Trp Ala Leu Pro Ile Thr His Thr Arg Lys Gln Leu Ala Glu Cys
 515 520 525
 Gln Lys His Leu Gly Gln Ile Glu Asn Tyr Leu Gln Thr Ser Ser Leu
 530 535 540
 Leu Ala Ser Asp His His Leu Thr Glu Glu Glu Arg Lys His Phe Cys
 545 550 555 560

Gln Glu Ile Leu Asp Phe Ala Ser Gln Pro Ser Asp Ser Pro Gly His
 565 570 575
 Lys Ile Val Leu Pro Met His Ser Phe Ala Gln Leu Arg Asp Leu His
 580 585 590
 Phe Asp Pro Ser Asn Ala Val Val His Val Gly Gly Val Leu Cys Val
 595 600 605
 Glu Ile Thr Met Tyr Ser Gln Met Pro Val Pro Val His Val Glu Gln
 610 615 620
 Ile Val Val Asn Val His Phe Ser Ile Glu Lys Asn Ser Tyr Arg Lys
 625 630 635 640
 Thr Ala Glu Trp Leu Thr Lys His Lys Thr Ser Asn Gly Ile Ile Asn
 645 650 655
 Phe Pro Pro Glu Thr Ala Pro Phe Pro Val Ser Gln Asn Ser Leu Pro
 660 665 670
 Ala Leu Glu Leu Tyr Glu Met Phe Glu Arg Ser Pro Ser Asp Asn Ser
 675 680 685
 Leu Asn Thr Thr Gly Ile Ile Cys Arg Asn Val His Met Leu Leu Arg
 690 695 700
 Arg Gln Glu Ser Ser Ser Leu Glu Met Pro Ser Gly Val Ala Leu
 705 710 715 720
 Glu Glu Gly Ala His Val Leu Arg Cys Ser His Val Thr Leu Glu Pro
 725 730 735
 Gly Ala Asn Gln Ile Thr Phe Arg Thr Gln Ala Lys Glu Pro Gly Thr
 740 745 750
 Tyr Thr Leu Arg Gln Leu Cys Ala Ser Val Gly Ser Val Trp Phe Val
 755 760 765
 Leu Pro His Ile Tyr Pro Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu
 770 775 780
 Pro Gln Leu His Val Glu Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile
 785 790 795 800
 Pro Gln Arg Val Lys Phe Thr Val Thr Gly His Asp Thr Ile Lys
 805 810 815
 Asn Gly Asp Ser Leu Gln Leu Ser Asn Ala Glu Ala Met Leu Ile Leu
 820 825 830
 Cys Gln Ala Glu Ser Arg Ala Val Val Tyr Ser Asn Thr Arg Glu Gln
 835 840 845
 Ser Ser Glu Ala Ala Leu Arg Ile Gln Ser Ser Asp Lys Val Thr Ser
 850 855 860
 Ile Ser Leu Pro Val Ala Pro Ala Tyr His Val Ile Glu Phe Glu Leu
 865 870 875 880
 Glu Val Leu Ser Leu Pro Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp
 885 890 895
 Met Leu Gly Met Ala Glu Pro His Arg Lys His Lys Asp Lys Gln Arg
 900 905 910

Thr Gly Arg Cys Met Val Thr Thr Asp His Lys Val Ser Ile Asp Cys
 915 920 925
 Pro Trp Ser Ile Tyr Ser Thr Val Ile Ala Leu Thr Phe Ser Val Pro
 930 935 940
 Phe Arg Thr Thr His Ser Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val
 945 950 955 960
 Gln Val Cys Val Gln Asn Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp
 965 970 975
 Ser Tyr Leu Val Asp Thr Gly Asp Ser Thr Asp Leu Gln Leu Val Pro
 980 985 990
 Leu Asn Thr Gln Ser Gln Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe
 995 1000 1005
 Phe Val Trp Glu Leu Lys Trp Thr Glu Glu Pro Pro Pro Ser Leu His
 1010 1015 1020
 Cys Arg Phe Ser Val Gly Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser
 1025 1030 1035 1040
 Ile Ser Leu Lys Pro Tyr Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe
 1045 1050 1055
 Thr Leu Tyr Asn Val Lys Ala Glu Ile Phe Pro Pro Ser Gly Met Glu
 1060 1065 1070
 Tyr Cys Arg Thr Gly Ser Leu Cys Ser Leu Glu Val Leu Ile Thr Arg
 1075 1080 1085
 Leu Ser Asp Leu Leu Glu Val Asp Lys Asp Glu Ala Leu Thr Glu Ser
 1090 1095 1100
 Asp Glu His Phe Ser Thr Lys Leu Met Tyr Glu Val Val Asp Asn Ser
 1105 1110 1115 1120
 Ser Asn Trp Ala Val Cys Gly Lys Ser Cys Gly Val Ile Ser Met Pro
 1125 1130 1135
 Val Ala Ala Arg Ala Thr His Arg Val His Met Glu Val Met Pro Leu
 1140 1145 1150
 Phe Ala Gly Tyr Leu Pro Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu
 1155 1160 1165
 Pro His His Ser Ala His Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile
 1170 1175 1180
 Glu Asn Ala Ala Cys Gln
 1185 1190

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella bovis*
- (C) INDIVIDUAL ISOLATE: *MboI* linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGATGCTC GAGTGAATT